



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/980,585A

DATE: 03/28/2002

TIME: 10:45:19

Input Set : N:\Crf3\03212002\I980585.raw

Output Set: N:\CRF3\03282002\I980585A.raw

1 <110> APPLICANT: LILIUS, Esa-Matti
 2 VIRTÄ, Marko
 3 <120> TITLE OF INVENTION: A Method to Enable Assessment of Growth and Death of Micro-organisms
 4 <130> FILE REFERENCE: 2328-124
 5 <140> CURRENT APPLICATION NUMBER: US/09/980,585A
 C--> 6 <141> CURRENT FILING DATE: 2000-06-07
 7 <150> PRIOR APPLICATION NUMBER: PCT/FI00/00507
 8 <151> PRIOR FILING DATE: 2000-06-07
 9 <150> PRIOR APPLICATION NUMBER: FI 991296
 10 <151> PRIOR FILING DATE: 1999-06-07
 11 <160> NUMBER OF SEQ ID NOS: 4
 12 <170> SOFTWARE: PatentIn version 3.0
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 15 <211> LENGTH: 5051
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
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 35 tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
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54	atacaaatca	cagaatcgtc	gtatgcagtg	aaaactctct	tcaattcttt	atgccgggtg	1320
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94 gacaacgatac ggaggaccga aggagctaac cgcttttttg cacaacatgg gggatcatgt 3720
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130 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
131 35 40 45
132 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
133 50 55 60
134 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
135 65 70 75 80
136 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
137 85 90 95
138 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
139 100 105 110
140 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
141 115 120 125
142 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
143 130 135 140

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144 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
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147 165 170 175
148 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
149 180 185 190
150 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
151 195 200 205
152 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
153 210 215 220
154 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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167 20 25 30
168 Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
169 35 40 45
170 Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
171 50 55 60
172 Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
173 65 70 75 80
174 Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
175 85 90 95
176 Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
177 100 105 110
178 Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val
179 115 120 125
180 Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
181 130 135 140
182 Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
183 145 150 155 160
184 Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
185 165 170 175
186 Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
187 180 185 190
188 Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
189 195 200 205
190 Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
191 210 215 220
192 Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
193 225 230 235 240

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198 Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
199                               275                               280                               285
200 Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
201                               290                               295                               300
202 Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
203                               305                               310                               315                               320
204 Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
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206 Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
207                               340                               345                               350
208 Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
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211                               370                               375                               380
212 Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
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214 Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
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216 Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
217                               420                               425                               430
218 Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
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226 Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
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228 Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
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238 <213> ORGANISM: Unknown
239 <220> FEATURE:
240 <223> OTHER INFORMATION: source of beta-lactamase unknown
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